



#6

SEQUENCE LISTING

<110> Gish, Kurt C.
Mack, David H.
Afar, Daniel
Eos Biotechnology, Inc.

<120> Uses of PBH1 in the Diagnosis and Therapeutic Treatment
of Prostate Cancer

<130> 018501-005910US

<140> US 10/058,513

<141> 2002-01-24

<150> US 60/263,951

<151> 2001-01-24

<160> 42

<170> PatentIn Ver. 2.1

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<211> 4225

<212> DNA

<213> Homo sapiens

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<212> PRT

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<223> prostate cancer modulating protein (PCMP) PBH1

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Ser	Phe	Leu	Pro	Val	His	Thr	Ile	Val	Leu	Ile	Arg	Glu	Asn	Val	Cys	50	55	60
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Gln	Ser	Glu	Lys	Trp	Asn	Tyr	Lys	Lys	His	Thr	Lys	Glu	Phe	Pro	Thr	85	90	95
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Tyr	Ile	Arg	Leu	Ser	Cys	Asp	Thr	Asp	Ala	Glu	Ile	Leu	Tyr	Glu	Leu	115	120	125
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Gly	Lys	Glu	Thr	Leu	Lys	Ala	Ile	Asn	Thr	Ser	Ile	Lys	Asn	Lys	Ile	305	310	315
Pro	Cys	Val	Val	Val	Glu	Gly	Ser	Gly	Gln	Ile	Ala	Asp	Val	Ile	Ala	325	330	335

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 Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu
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 370 375 380
 His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val
 385 390 395 400
 Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu
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 Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg
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 Trp Leu Glu Asn Gly Arg Ile Lys Val Glu Ser Lys Asp Val Thr Asp
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 Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu
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 Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala
 625 630 635 640
 Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala
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 Ser Val Thr Gly Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg Met Arg
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 Ala Ile Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp Thr Leu
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Ile	Ala	Ser	Leu	Val	Glu	Val	Glu	Asp	Ala	Leu	Thr	Ser	Ser	Ala	Val	
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 515 520 525
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 580 585 590
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 595 600 605
 Tyr Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys
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 peptide sequence

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 35 40 45
 Ser Gln Lys Val Lys Lys Tyr Val Arg Val Ser Gln Asp Thr Pro Ser
 50 55 60
 Ser Val Ile Tyr His Leu Met Thr Gln His Trp Gly Leu Asp Val Pro
 65 70 75 80

Asn	Leu	Leu	Ile	Ser	Val	Thr	Gly	Gly	Ala	Lys	Asn	Phe	Asn	Met	Lys	85	90	95
Pro	Arg	Leu	Lys	Ser	Ile	Phe	Arg	Arg	Gly	Leu	Val	Lys	Val	Ala	Gln	100	105	110
Thr	Thr	Gly	Ala	Trp	Ile	Ile	Thr	Gly	Gly	Ser	His	Thr	Gly	Val	Met	115	120	125
Lys	Gln	Val	Gly	Glu	Ala	Val	Arg	Asp	Phe	Ser	Leu	Ser	Ser	Ser	Tyr	130	135	140
Lys	Glu	Gly	Glu	Leu	Ile	Thr	Ile	Gly	Val	Ala	Thr	Trp	Gly	Thr	Val	145	150	155
His	Arg	Arg	Glu	Gly	Leu	Ile	His	Pro	Thr	Gly	Ser	Phe	Pro	Ala	Glu	165	170	175
Tyr	Ile	Leu	Asp	Glu	Asp	Gly	Gln	Gly	Asn	Leu	Thr	Cys	Leu	Asp	Ser	180	185	190
Asn	His	Ser	His	Phe	Ile	Leu	Val	Asp	Asp	Gly	Thr	His	Gly	Gln	Tyr	195	200	205
Gly	Val	Glu	Ile	Pro	Leu	Arg	Thr	Arg	Leu	Glu	Lys	Phe	Ile	Ser	Glu	210	215	220
Gln	Thr	Lys	Glu	Arg	Gly	Gly	Val	Ala	Ile	Lys	Ile	Pro	Ile	Val	Cys	225	230	235
Val	Val	Leu	Glu	Gly	Gly	Pro	Gly	Thr	Leu	His	Thr	Ile	Asp	Asn	Ala	245	250	255
Thr	Thr	Asn	Gly	Thr	Pro	Cys	Val	Val	Val	Glu	Gly	Ser	Gly	Arg	Val	260	265	270
Ala	Asp	Val	Ile	Ala	Gln	Val	Ala	Asn	Leu	Pro	Val	Ser	Asp	Ile	Thr	275	280	285
Ile	Ser	Leu	Ile	Gln	Gln	Lys	Leu	Ser	Val	Phe	Phe	Gln	Glu	Met	Phe	290	295	300
Glu	Thr	Phe	Thr	Glu	Ser	Arg	Ile	Val	Glu	Trp	Thr	Lys	Lys	Ile	Gln	305	310	315
Asp	Ile	Val	Arg	Arg	Arg	Gln	Leu	Leu	Thr	Val	Phe	Arg	Glu	Gly	Lys	325	330	335
Asp	Gly	Gln	Gln	Asp	Val	Asp	Val	Ala	Ile	Leu	Gln	Ala	Leu	Leu	Lys	340	345	350
Ala	Ser	Arg	Ser	Gln	Asp	His	Phe	Gly	His	Glu	Asn	Trp	Asp	His	Gln	355	360	365
Leu	Lys	Leu	Ala	Val	Ala	Trp	Asn	Arg	Val	Asp	Ile	Ala	Arg	Ser	Glu	370	375	380
Ile	Phe	Met	Asp	Glu	Trp	Gln	Trp	Lys	Pro	Ser	Asp	Leu	His	Pro	Thr	385	390	395

Met Thr Ala Ala Leu Ile Ser Asn Lys Pro Glu Phe Val Lys Leu Phe
 405 410 415
 Leu Glu Asn Gly Val Gln Leu Lys Glu Phe Val Thr Trp Asp Thr Leu
 420 425 430
 Leu Tyr Leu Tyr Glu Asn Leu Asp Pro Ser Cys Leu Phe His Ser Lys
 435 440 445
 Leu Gln Lys Val Leu Val Glu Asp Pro Glu Arg Pro Ala Cys Ala Pro
 450 455 460
 Ala Ala Pro Arg Leu Gln Met His His Val Ala Gln Val Leu Arg Glu
 465 470 475 480
 Leu Leu Gly Asp Phe Thr Gln Pro Leu Tyr Pro Arg Pro Arg His Asn
 485 490 495
 Asp Arg Leu Arg Leu Leu Leu Pro Val Pro His Val Lys Leu Asn Val
 500 505 510
 Gln Gly Val Ser Leu Arg Ser Leu Tyr Lys Arg Ser Ser Gly His Val
 515 520 525
 Thr Phe Thr Met Asp Pro Ile Arg Asp Leu Leu Ile Trp Ala Ile Val
 530 535 540
 Gln Asn Arg Arg Glu Leu Ala Gly Ile Ile Trp Ala Gln Ser Gln Asp
 545 550 555 560
 Cys Ile Ala Ala Ala Leu Ala Cys Ser Lys Ile Leu Lys Glu Leu Ser
 565 570 575
 Lys Glu Glu Glu Asp Thr Asp Ser Ser Glu Glu Met Leu Ala Leu Ala
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 Glu Glu Tyr Glu His Arg Ala Ile Gly Val Phe Thr Glu Cys Tyr Arg
 595 600 605
 Lys Asp Glu Glu Arg Ala Gln Lys Leu Leu Thr Arg Val Ser Glu Ala
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<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

<400> 5

Pro Thr Asp Ala Phe Gly Asp Ile

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5

<210> 6
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 6
 Thr Gln His Trp
 1

<210> 7
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 7
 Ile Ser Val Thr Gly Gly Ala Lys Asn Phe
 1 5 10

<210> 8
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 8
 Gly Ala Trp Ile
 1

<210> 9
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 9
 Lys Ile Pro Ile Val Cys
 1 5

<210> 10
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
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peptide sequence from PBH1 and TRPC7 alignment

<400> 10
Pro Cys Val Val Val Glu Gly Ser Gly
1 5

<210> 11
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 11
Ala Asp Val Ile Ala
1 5

<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 12
Leu Leu Thr Val
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<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 13
Gln Leu Lys Leu
1

<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 14
Leu Phe Leu Glu Asn Gly
1 5

<210> 15
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 15
Ile Trp Ala Ile
1

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 16
Phe Thr Glu Cys Tyr
1 5

<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide sequence from PBH1 and TRPC7 alignment

<400> 17
Glu Ala Trp Gly
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<210> 18
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PBH1 peptide
sequence

<400> 18
Ala Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe
1 5 10 15

Tyr Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe
 20 25 30

His Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe
 35 40 45

Val Leu Phe Cys Asp Glu Val Arg Gln
 50 55

<210> 19
 <211> 57
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:transient
 receptor potential-related channel 7 (TRPC7)
 peptide sequence

<400> 19
 Ala Phe Phe Thr Ala Pro Val Val Val Phe His Leu Asn Ile Leu Ser
 1 5 10 15

Tyr Phe Ala Phe Leu Cys Leu Phe Ala Tyr Val Leu Met Val Asp Phe
 20 25 30

Gln Pro Val Pro Ser Trp Cys Glu Cys Ala Ile Tyr Leu Trp Leu Phe
 35 40 45

Ser Leu Val Cys Glu Glu Met Arg Gln
 50 55

<210> 20
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

<400> 20
 Ala Phe Phe Thr
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<210> 21
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

<400> 21
 Leu Phe Ala Tyr Val Leu
 1 5

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<210> 22
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PBH1 peptide
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<220>
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<222> (77)..(82)
<223> Xaa = low complexity amino acid from BLASTP search

<400> 22
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Phe Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser
      20             25             30

Leu Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr
      35             40             45

Leu Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys
      50             55             60

Ile Ile Met Leu Gln Arg Met Thr Ser Ile Glu Met Xaa Xaa Xaa Xaa
      65             70             75             80

Xaa Xaa Ile Pro Thr Leu Arg Phe Phe Glu Phe Val Val Leu Ile Gln
      85             90             95

Ser Ile Ser Gly Thr Ser Ser His His Glu Val Met Leu Ser Asp Arg
      100            105            110

Cys Val Leu Leu Pro Val Pro Leu Cys Gly Val Asp Gly Gly Leu Cys
      115            120            125

Val Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp Arg Trp
      130            135            140

Ile Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe Gly Gln
      145            150            155            160

Val Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His Cys Thr
      165            170            175

Phe Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp Glu His
      180            185            190

Asn Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val Cys Ile
      195            200            205

Tyr Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val Ala Met
      210            215            220

Phe
225

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<210> 23
 <211> 186
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:transient
 receptor potential-related channel 7 (TRPC7)
 peptide sequence

<400> 23
 Tyr Phe Ser Asp Phe Trp Asn Lys Leu Asp Val Gly Ala Ile Leu Leu
 1 5 10 15
 Phe Val Ala Gly Leu Thr Cys Arg Leu Ile Pro Ala Thr Leu Tyr Pro
 20 25 30
 Gly Arg Val Ile Leu Ser Leu Asp Phe Ile Leu Phe Cys Leu Arg Leu
 35 40 45
 Met His Ile Phe Thr Ile Ser Lys Thr Leu Gly Pro Lys Ile Ile Ile
 50 55 60
 Val Lys Arg Met Met Lys Asp Val Phe Phe Phe Leu Phe Leu Leu Ala
 65 70 75 80
 Val Trp Val Val Ser Phe Gly Val Ala Lys Gln Ala Ile Leu Ile His
 85 90 95
 Asn Glu Arg Arg Val Asp Trp Leu Phe Arg Gly Ala Val Tyr His Ser
 100 105 110
 Tyr Leu Thr Ile Phe Gly Gln Ile Pro Gly Tyr Ile Asp Gly Val Asn
 115 120 125
 Phe Asn Pro Glu His Cys Ser Pro Asn Gly Thr Asp Pro Tyr Lys Pro
 130 135 140
 Lys Cys Pro Glu Ser Asp Ala Thr Gln Gln Arg Pro Ala Phe Pro Glu
 145 150 155 160
 Trp Leu Thr Val Leu Leu Leu Cys Leu Tyr Leu Leu Phe Thr Asn Ile
 165 170 175
 Leu Leu Leu Asn Leu Leu Ile Ala Met Phe
 180 185

<210> 24
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

<400> 24
 Gly Arg Val Ile
 1

<210> 25
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 25
 His Ile Phe Thr
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<210> 26
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 26
 Leu Gly Pro Lys Ile Ile
 1 5

<210> 27
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 27
 Phe Pro Glu Trp
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<210> 28
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence from PBH1 and TRPC7 alignment

 <400> 28
 Thr Asn Ile Leu Leu
 1 5

<210> 29
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PBH1 peptide
 sequence

<400> 29
 Tyr Thr Val Gly Thr Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe
 1 5 10 15
 Gln Arg Tyr Phe Leu Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro
 20 25 30
 Phe Pro Phe Ile Val Phe Ala Tyr Phe Tyr Met Val Val
 35 40 45

<210> 30
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:transient
 receptor potential-related channel 7 (TRPC7)
 peptide sequence

<400> 30
 Tyr Thr Phe Gln Gln Val Gln Glu His Thr Asp Gln Ile Trp Lys Phe
 1 5 10 15
 Gln Arg His Asp Leu Ile Glu Glu Tyr His Gly Arg Pro Ala Ala Pro
 20 25 30
 Pro Pro Phe Ile Leu Leu Ser His Leu Gln Leu Phe Ile
 35 40 45

<210> 31
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide sequence for PBH1 and TRPC7 alignment

<400> 31
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 1 5

<210> 32
 <211> 2181
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exons 1-15 of PBH1

<400> 32
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<210> 33
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 16 of PBH1

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<210> 34
 <211> 1761
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exons 17-28 of PBH1

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<400> 34
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<210> 35
<211> 713
<212> PRT
<213> Homo sapiens

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<220>
<223> exons 1-15 of PBH1

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<400> 35
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Gly Asp Val Val Gly Ser Arg Ser Pro Gln Gln His Lys Arg Ser Thr
      20             25             30

Gly Thr Pro Gln Gly Leu Pro Val Pro Ile Ser Glu Gly Ser Met Lys
      35             40             45

Ser Phe Leu Pro Val His Thr Ile Val Leu Ile Arg Glu Asn Val Cys
      50             55             60

Lys Cys Gly Tyr Ala Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn
      65             70             75             80

Gln Ser Glu Lys Trp Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr
      85             90             95

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Asp	Ala	Phe	Gly	Asp	Ile	Gln	Phe	Glu	Thr	Leu	Gly	Lys	Lys	Gly	Lys	100	105	110	
Tyr	Ile	Arg	Leu	Ser	Cys	Asp	Thr	Asp	Ala	Glu	Ile	Leu	Tyr	Glu	Leu	115	120	125	
Leu	Thr	Gln	His	Trp	His	Leu	Lys	Thr	Pro	Asn	Leu	Val	Ile	Ser	Val	130	135	140	
Thr	Gly	Gly	Ala	Lys	Asn	Phe	Ala	Leu	Lys	Pro	Arg	Met	Arg	Lys	Ile	145	150	155	160
Phe	Ser	Arg	Leu	Ile	Tyr	Ile	Ala	Gln	Ser	Lys	Gly	Ala	Trp	Ile	Leu	165	170	175	
Thr	Gly	Gly	Thr	His	Tyr	Gly	Leu	Met	Lys	Tyr	Ile	Gly	Glu	Val	Val	180	185	190	
Arg	Asp	Asn	Thr	Ile	Ser	Arg	Ser	Ser	Glu	Glu	Asn	Ile	Val	Ala	Ile	195	200	205	
Gly	Ile	Ala	Ala	Trp	Gly	Met	Val	Ser	Asn	Arg	Asp	Thr	Leu	Ile	Arg	210	215	220	
Asn	Cys	Asp	Ala	Glu	Gly	Tyr	Phe	Leu	Ala	Gln	Tyr	Leu	Met	Asp	Asp	225	230	235	240
Phe	Thr	Arg	Asp	Pro	Leu	Tyr	Ile	Leu	Asp	Asn	Asn	His	Thr	His	Leu	245	250	255	
Leu	Leu	Val	Asp	Asn	Gly	Cys	His	Gly	His	Pro	Thr	Val	Glu	Ala	Lys	260	265	270	
Leu	Arg	Asn	Gln	Leu	Glu	Lys	Tyr	Ile	Ser	Glu	Arg	Thr	Ile	Gln	Asp	275	280	285	
Ser	Asn	Tyr	Gly	Gly	Lys	Ile	Pro	Ile	Val	Cys	Phe	Ala	Gln	Gly	Gly	290	295	300	
Gly	Lys	Glu	Thr	Leu	Lys	Ala	Ile	Asn	Thr	Ser	Ile	Lys	Asn	Lys	Ile	305	310	315	320
Pro	Cys	Val	Val	Val	Glu	Gly	Ser	Gly	Gln	Ile	Ala	Asp	Val	Ile	Ala	325	330	335	
Ser	Leu	Val	Glu	Val	Glu	Asp	Ala	Leu	Thr	Ser	Ser	Ala	Val	Lys	Glu	340	345	350	
Lys	Leu	Val	Arg	Phe	Leu	Pro	Arg	Thr	Val	Ser	Arg	Leu	Pro	Glu	Glu	355	360	365	
Glu	Thr	Glu	Ser	Trp	Ile	Lys	Trp	Leu	Lys	Glu	Ile	Leu	Glu	Cys	Ser	370	375	380	
His	Leu	Leu	Thr	Val	Ile	Lys	Met	Glu	Glu	Ala	Gly	Asp	Glu	Ile	Val	385	390	395	400
Ser	Asn	Ala	Ile	Ser	Tyr	Ala	Leu	Tyr	Lys	Ala	Phe	Ser	Thr	Ser	Glu	405	410	415	

Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp
 420 425 430
 Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg
 435 440 445
 Trp Glu Lys Ser Lys Pro Arg Leu Arg Asp Thr Ile Ile Gln Val Thr
 450 455 460
 Trp Leu Glu Asn Gly Arg Ile Lys Val Glu Ser Lys Asp Val Thr Asp
 465 470 475 480
 Gly Lys Ala Ser Ser His Met Leu Val Val Leu Lys Ser Ala Asp Leu
 485 490 495
 Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe Val
 500 505 510
 Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr His
 515 520 525
 Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val Tyr
 530 535 540
 Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr
 545 550 555 560
 Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu
 565 570 575
 Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val Ser
 580 585 590
 Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu
 595 600 605
 Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg Gly
 610 615 620
 Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala
 625 630 635 640
 Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala
 645 650 655
 Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr Ser
 660 665 670
 Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu Ala
 675 680 685
 Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp Gln
 690 695 700
 His Phe Ile Ala Gln Pro Gly Val Gln
 705 710

<210> 36
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <223> exon 16 of PBH1

<400> 36
 Arg Gly Gly Leu Cys Pro Ser His Ala Cys Lys Asp Ala Asp Asp Ala
 1 5 10 15
 Leu Ile Ser Gly Ser Arg Lys Lys Pro Val Asp Lys His Lys Lys Leu
 20 25 30
 Leu Trp Tyr Tyr Val Ala Phe Phe Thr Ser Pro Phe Val Val Phe Ser
 35 40 45
 Trp Asn Val Val Phe Tyr Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val
 50 55 60
 Leu Leu Met Asp Phe His Ser Val Pro His Pro Pro Glu Leu Val Leu
 65 70 75 80
 Tyr Ser Leu Val Phe Val Leu Phe Cys Asp Glu Val Arg Gln
 85 90

<210> 37
 <211> 586
 <212> PRT
 <213> Homo sapiens

<220>
 <223> exons 17-28 of PBH1

<400> 37
 Met Glu Gln Gly Val Ala Leu Val Glu Glu Ala Arg Ala Ala Gln Glu
 1 5 10 15
 Pro Thr Glu Gly Val Gly Gly Ser Gly Met Val Gly Cys Arg Ser Arg
 20 25 30
 Ala Leu Pro His Gly Lys Ala Ala Thr Ala Arg Pro Gly Ser Arg Ser
 35 40 45
 Arg His Ser Phe His Thr Ser Leu Gln Ala Glu Gly Ala Ser Ser Gly
 50 55 60
 Leu Gly Gln Pro Arg Lys Gly Leu Pro Gln Cys Ser Gly Gly Leu Lys
 65 70 75 80
 Gly Ser Ser Ser Ala Ala Lys Val Gly Ala Gln Ala Glu Glu Val Pro
 85 90 95
 Arg Ala Ser Glu Gly Cys Glu Asp Cys Gln His Ala Val Thr Ser Gln
 100 105 110
 Lys Arg Lys Gly Leu Ala Asp Val Leu Ser Arg Thr Gly Asn Asn Trp
 115 120 125

Asp	Ser	Val	Cys	Pro	Thr	Ser	Gly	Trp	Tyr	Val	Asn	Gly	Val	Asn	Tyr	130	135	140
Phe	Thr	Asp	Leu	Trp	Asn	Val	Met	Asp	Thr	Leu	Gly	Leu	Phe	Tyr	Phe	145	150	155
Ile	Ala	Gly	Ile	Val	Phe	Arg	Leu	His	Ser	Ser	Asn	Lys	Ser	Ser	Leu	165	170	175
Tyr	Ser	Gly	Arg	Val	Ile	Phe	Cys	Leu	Asp	Tyr	Ile	Ile	Phe	Thr	Leu	180	185	190
Arg	Leu	Ile	His	Ile	Phe	Thr	Val	Ser	Arg	Asn	Leu	Gly	Pro	Lys	Ile	195	200	205
Ile	Met	Leu	Gln	Arg	Met	Thr	Ser	Ile	Glu	Met	Ser	Ser	Ser	Gly	Ser	210	215	220
Ser	Ile	Pro	Thr	Leu	Arg	Phe	Phe	Glu	Phe	Val	Val	Leu	Ile	Gln	Ser	225	230	235
Ile	Ser	Gly	Thr	Ser	Ser	His	His	Glu	Val	Met	Leu	Ser	Asp	Arg	Cys	245	250	255
Val	Leu	Leu	Pro	Val	Pro	Leu	Cys	Gly	Val	Asp	Gly	Gly	Leu	Cys	Val	260	265	270
Ala	Arg	Gln	Gly	Ile	Leu	Arg	Gln	Asn	Glu	Gln	Arg	Trp	Arg	Trp	Ile	275	280	285
Phe	Arg	Ser	Val	Ile	Tyr	Glu	Pro	Tyr	Leu	Ala	Met	Phe	Gly	Gln	Val	290	295	300
Pro	Ser	Asp	Val	Asp	Gly	Thr	Thr	Tyr	Asp	Phe	Ala	His	Cys	Thr	Phe	305	310	315
Thr	Gly	Asn	Glu	Ser	Lys	Pro	Leu	Cys	Val	Glu	Leu	Asp	Glu	His	Asn	325	330	335
Leu	Pro	Arg	Phe	Pro	Glu	Trp	Ile	Thr	Ile	Pro	Leu	Val	Cys	Ile	Tyr	340	345	350
Met	Leu	Ser	Thr	Asn	Ile	Leu	Leu	Val	Asn	Leu	Leu	Val	Ala	Met	Phe	355	360	365
Gly	Cys	Val	Ala	Gly	Gly	Leu	Val	Gln	Val	Leu	Asp	Phe	Gly	Thr	Glu	370	375	380
Asn	Asn	Leu	Lys	Val	Ser	Gln	Lys	Gln	Lys	Gln	Ala	Arg	Glu	Leu	Thr	385	390	395
Ala	Lys	Pro	Lys	Tyr	Thr	Leu	Ala	Ala	Ala	Gly	Phe	Arg	Arg	Trp	Thr	405	410	415
Ser	Ala	Val	Thr	Ala	Cys	Leu	Gln	Pro	Ala	Arg	Cys	Leu	Pro	Gly	Thr	420	425	430
Gly	Arg	Gln	Gly	His	Lys	Ile	Ser	Leu	Glu	Met	His	Lys	Gly	Lys	Ile	435	440	445

Ala Glu Phe Ser Gln Gly Gln His Gln Met Ala Thr Gly Cys Gln Gly
 450 455 460
 Asp Phe Lys Asn His Leu Arg Trp Gly Gly Tyr Thr Val Gly Thr Val
 465 470 475 480
 Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu Val
 485 490 495
 Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val Phe
 500 505 510
 Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys Lys
 515 520 525
 Glu Lys Asn Met Glu Ser Ser Val Cys Ser Val Glu Ala Gly Glu Asp
 530 535 540
 Ala Tyr Asn Tyr Arg Glu His Lys Glu Gly Ser Lys Glu Leu Phe Gly
 545 550 555 560
 Ser Gln Cys Ala Leu Met Leu Val Phe Ala Ala Thr Leu Ile Arg Cys
 565 570 575
 Leu Phe Tyr Leu Glu Gly Ile Gly Asn Ala
 580 585

<210> 38
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:cytokine
 receptor transmembrane protein extracellular
 domain conserved motif

<220>
 <221> MOD_RES
 <222> (3)
 <223> Xaa = any amino acid

<400> 38
 Trp Ser Xaa Trp Ser
 1 5

<210> 39
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:T7-(dT)-24
 primer

<400> 39
 tttttttttt tttttttttt tttt

<210> 40
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amino acids
 168-180 from PBH1 exons 17-28, extracellular
 region used to generate therapeutic antibodies

<400> 40
 Leu His Ser Ser Asn Lys Ser Ser Leu Tyr Ser Gly Arg
 1 5 10

<210> 41
 <211> 68
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amino acids
 274-342 from PBH1 exons 17-28, extracellular
 region used to generate therapeutic antibodies

<400> 41
 Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe
 1 5 10 15
 Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro
 20 25 30
 Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr
 35 40 45
 Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu
 50 55 60
 Pro Arg Phe Pro
 65

<210> 42
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amino acids
 520-560 from PBH1 exons 17-28, extracellular
 region used to generate therapeutic antibodies

<400> 42
 Lys Lys Cys Phe Lys Cys Cys Cys Lys Glu Lys Asn Met Glu Ser Ser
 1 5 10 15
 Val Cys Ser Val Glu Ala Gly Glu Asp Ala Tyr Asn Tyr Arg Glu His
 20 25 30
 Lys Glu Gly Ser Lys Glu Leu Phe Gly
 35 40